

**ABSTRACT**

Expression profiling using DNA microarrays is an important new method for analyzing cellular physiology. In “spotted” microarrays, fluorescently labeled cDNA from experimental and control cells is hybridized to arrayed target DNA and the arrays imaged at two or more wavelengths. Statistical analysis is performed on microarray images and show that non-additive background, high intensity fluctuations across spots, and fabrication artifacts interfere with the accurate determination of intensity information. The probability density distributions generated by pixel-by-pixel analysis of images can be used to measure the precision with which spot intensities are determined. Simple weighting schemes based on these probability distributions are effective in improving significantly the quality of microarray data as it accumulates in a multi-experiment database. Error estimates from image-based metrics should be one component in an explicitly probabilistic scheme for the analysis of DNA microarray data.

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